

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search  for

Show:

☐ 1: AAD02832. raffinose synthas...[gi:4106395]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAD02832 784 aa linear PLN 05-JAN-1999  
DEFINITION raffinose synthase [Cucumis sativus].  
ACCESSION AAD02832  
VERSION AAD02832.1 GI:4106395  
DBSOURCE locus AF073744 accession [AF073744.1](#)  
KEYWORDS .  
SOURCE Cucumis sativus (cucumber)  
ORGANISM Cucumis sativus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
REFERENCE 1 (residues 1 to 784)  
AUTHORS Ohsumi,C., Nozaki,J. and Kida,T.  
TITLE Direct Submission  
JOURNAL Submitted (22-JUN-1998) Central Research Laboratories, Aajinomoto  
Co. Inc., 1-1, Suzuki-cho, Kawasaki-ku, Kawasaki 210-8681, Japan  
COMMENT Method: conceptual translation supplied by author.  
FEATURES Location/Qualifiers  
source 1..784  
/organism="Cucumis sativus"  
/db\_xref="taxon:3659"  
/tissue\_type="leaf"  
/dev\_stage="mature"  
Protein 1..784  
/product="raffinose synthase"  
/EC\_number="2.4.1.82"  
CDS 1..784  
/gene="Rfs"  
/coded\_by="AF073744.1:56..2410"

#### ORIGIN

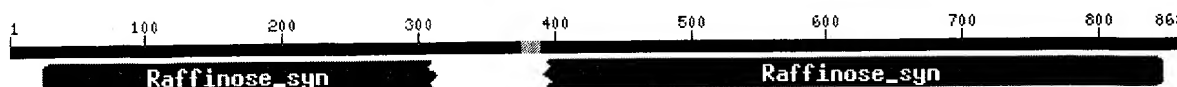
```
1 mapsfknngs nvvsfdglnd msspfaidgs dftvnghsfl sdvpenivas pspytsidks
61 pvsvgcfvgf dasepdsrhv vsigklkdir fmsifrkvw wtthwvgrng gdlesetqiv
121 ileksdsgvp yvflpiveg pfrtsiqpgd ddfvdvcves gsskvvdasf rsmlylhagd
181 dpfalvkeam kivrthlgtf rlleektppg ivdkfgwctw dafyltvhpq gviegvrhlv
241 dggcppglvl iddgwqsigh dsdpitkegm nqtvageqmp crllkfgeny kfrdyvnpka
301 tgpragqkgm kafidelkge fktvehvyvw halcgywggf rpqvpplpea rviqpvlspg
361 lqmtmedlav dkiavlkhvgl vppekaeemy eglhahlekv gidgvkidvi hllemlcedy
421 ggrvdlakay ykamtksink hfkngnvias mehcndfmfl gteaislgrv gddfwctdps
481 gdpngtflwq gchmvhcand slwmgnfihp dwdmfqsthp caafhaasra isggpiyvsv
541 svgkhnfdll kklvlpdgsi lrseyyalpt rdclfedplh ngetmlkiwn lnkftgviga
601 fncqgggwcr etrrnqcfsg yskrvtsktn pkdiewhsge npisiegvkt falylyqakk
661 lilskpsqdl dialdpfefe litvspvtnl iqtshlfapi glvnmlntsg aqsvdyddd
721 lssveigvkg cgemrvfask kpracridge dvgfkydqdq mvvvqvpwpi dsssggisvi
781 eylf
```

//

Your request has been successfully submitted and put into the Blast Queue.

Query = gi|19571727 (863 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is 1084294765-17791-93877873360.BLASTQ3

**Format!** or **Reset all**

The results are estimated to be ready in 48 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

### Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi Alignment  in  HTML

Use new formatter ☐ Masking Character: Default(X for protein, n for nucleotide)  Masking Color: Black

Number of: Descriptions: 100  Alignments: 50

Alignment view: Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by entrez query:  or select from: All organisms

Expect value range:



# results of BLAST

BLASTP 2.2.9 [May-01-2004]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1084294765-17791-93877873360.BLASTQ3

Query= gi|19571727|emb|CAC86963.1| stachyose synthase [Stachys affinis]

(863 letters)

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

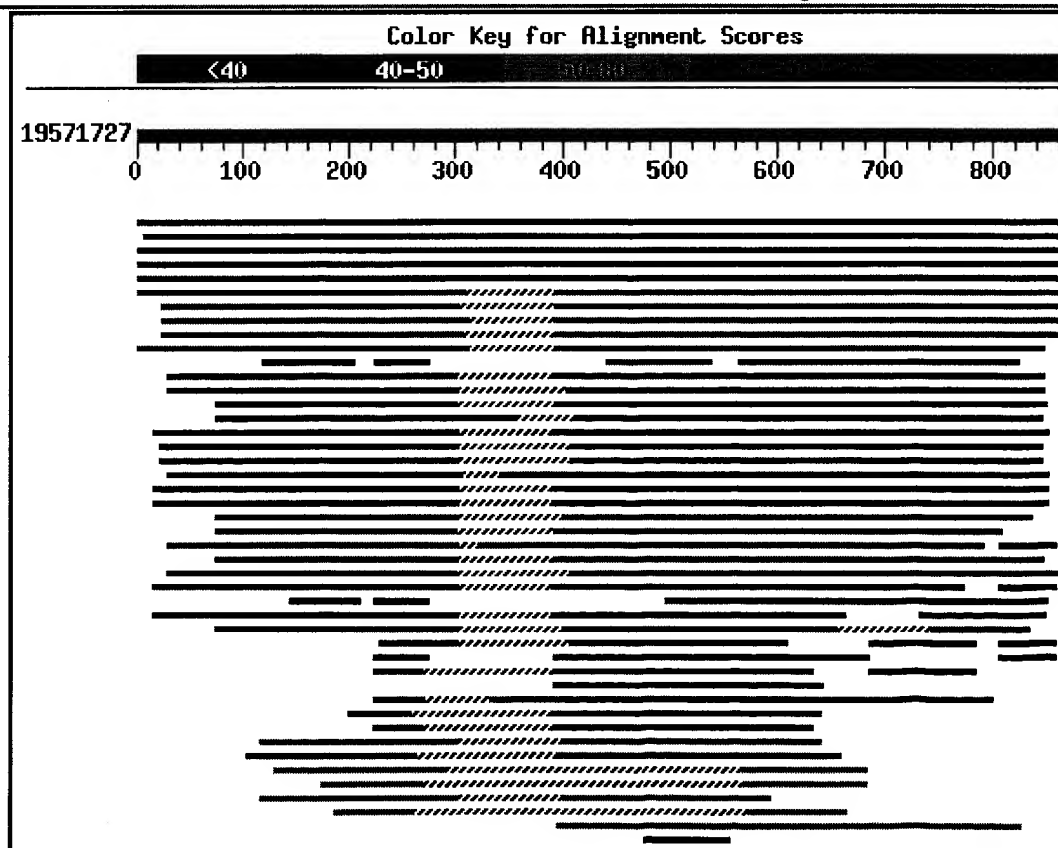
1,798,171 sequences; 593,787,773 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 93 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



## Sequences producing significant alignments:

Score E  
(bits) Value

gi	6634701	emb	CAB64363.1	galactinol-raffinose galactosylt...	1204	0.0	
gi	21038869	emb	CAD31704.1	putative stachyose synthase [Al...	1426	0.0	
gi	13992585	emb	CAC38094.1	stachyose synthase [Pisum sativum]	1181	0.0	
gi	24412857	emb	CAD55555.1	stachyose synthase [Pisum sativum]	1183	0.0	
gi	19571727	emb	CAC86963.1	stachyose synthase [Stachys aff...	1759	0.0	
gi	15235191	ref	NP 192106.1	galactinol-raffinose galactosy...	639	0.0	
gi	15242680	ref	NP 198855.1	raffinose synthase family prot...	518	e-145	
gi	4106395	gb	AAD02832.1	raffinose synthase [Cucumis sativus]	506	e-141	
gi	34896196	ref	NP 909442.1	putative raffinose synthase [O...	493	e-138	
gi	18181865	emb	CAD20127.2	raffinose synthase [Pisum sativum]	489	e-137	
gi	39841611	gb	AAR31209.1	stachyose synthase [Medicago sat...	428	e-118	
gi	282994	pir	S27762 Sip1	protein - barley >gi 167100 gb A...	344	4e-93	
gi	23452226	gb	AAN32954.1	alkaline alpha-galactosidase see...	338	2e-91	
gi	42408863	dbj	BAD10122.1	putative alkaline alpha-galacto...	328	3e-88	
gi	29838629	gb	AAM75139.1	alkaline alpha galactosidase I [...]	326	1e-87	
gi	629602	pir	S45033	probable imbibition protein - wild ca...	322	2e-86	
gi	30687712	ref	NP 851044.1	raffinose synthase family prot...	322	3e-86	
gi	15241300	ref	NP 197525.1	raffinose synthase family prot...	321	6e-86	
gi	34393428	dbj	BAC82968.1	putative Sip1 protein [Oryza sa...	314	5e-84	
gi	15292677	gb	AAK92707.1	putative imbibition protein homo...	313	1e-83	
gi	15230330	ref	NP 191311.1	alkaline alpha galactosidase, ...	313	1e-83	
gi	15222768	ref	NP 175970.1	alkaline alpha galactosidase, ...	311	5e-83	
gi	42408862	dbj	BAD10121.1	putative alkaline alpha-galacto...	310	9e-83	
gi	29838631	gb	AAM75140.1	alkaline alpha galactosidase II ...	298	3e-79	
gi	7242785	emb	CAB77245.1	putative seed imbibition protein...	289	1e-76	
gi	38345247	emb	CAD41091.2	OSJNBb0011N17.8 [Oryza sativa (...]	281	4e-74	
gi	30694660	ref	NP 850715.1	alkaline alpha galactosidase, ...	278	3e-73	
gi	6850938	emb	CAB71135.1	putative imbibition protein [Cic...	227	8e-58	
gi	42572711	ref	NP 974451.1	alkaline alpha galactosidase, ...	214	7e-54	
gi	25405998	pir	C96599	protein F20N2.14 [imported] - Arabi...	188	4e-46	
gi	10834552	gb	AAG23721.1	seed imbibition protein [Arabido...	138	6e-31	
gi	32422611	ref	XP 331749.1	hypothetical protein [Neurospo...	107	1e-21	
gi	46107958	ref	XP 381038.1	hypothetical protein FG00862.1...	102	3e-20	
gi	38105598	gb	EAA52006.1	hypothetical protein MG03601.4 [...]	100	2e-19	
gi	38102033	gb	EAA48924.1	hypothetical protein MG00582.4 [...]	100	2e-19	
gi	7488636	pir	T09530	probable seed inhibition protein - c...	97	1e-18	
gi	40739949	gb	EAA59139.1	hypothetical protein AN3874.2 [A...	89	4e-16	
gi	7485235	pir	T01717	hypothetical protein A_IG002N01.5 - ...	83	3e-14	
gi	42565254	gb	AAK96217.2	alpha-galactosidase [Bifidobacte...	82	4e-14	
gi	18201643	gb	AAL65392.1	putative seed imbibition protein...	81	1e-13	
gi	15922888	ref	NP 378557.1	674aa long hypothetical sip1 p...	72	7e-11	
gi	15899832	ref	NP 344437.1	Raffinose synthase (Sip1 seed ...	70	3e-10	
gi	22328210	ref	NP 680552.1	raffinose synthase family prot...	65	9e-09	
gi	29349205	ref	NP 812708.1	conserved hypothetical protein...	60	3e-07	
gi	46095960	gb	EAK81193.1	hypothetical protein UM00375.1 [...]	55	6e-06	
gi	37535242	ref	NP 921923.1	putative stachyose synthase [O...	49	4e-04	
gi	42560413	gb	AAS20373.1	HrpS [Pectobacterium atrosepticum]	37	1.4	
gi	34500866	gb	AAQ73894.1	HrpS [Pectobacterium carotovorum...	37	2.3	
gi	37679563	ref	NP 934172.1	alpha-galactosidase [Vibrio vu...	37	2.7	
gi	13569928	ref	NP 112217.1	a disintegrin-like and metallo...	36	3.4	L
gi	27904866	ref	NP 777992.1	guanylate kinase [Buchnera aph...	36	3.6	
gi	27366169	ref	NP 761697.1	Alpha-galactosidase [Vibrio vu...	36	3.8	
gi	26339440	dbj	BAC33391.1	unnamed protein product [Mus mu...	36	4.3	L
gi	18978155	ref	NP 579512.1	molybdenum cofactor biosynthes...	36	4.3	
gi	15213600	gb	AAK92078.1	glycoprotein [rabies virus]	35	5.4	
gi	29789429	ref	NP 780710.1	a disintegrin-like and metallo...	35	5.6	L
gi	34854396	ref	XP 226837.2	similar to metalloprotease dis...	35	6.2	L



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search

Protein

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

default

Show:

20

Send to

File

Get Subsequence

Features

1: CAC86963. stachyose synthas...[gi:19571727]

BLink, Domains, Links

LOCUS CAC86963 863 aa linear PLN 13-MAR-2002

DEFINITION stachyose synthase [Stachys affinis].

ACCESSION CAC86963

VERSION CAC86963.1 GI:19571727

DBSOURCE embl locus SSI344091, accession AJ344091.1

KEYWORDS .

SOURCE Stachys affinis

ORGANISM Stachys affinis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiids; Lamiales; Lamiaceae; Lamioideae; Stachys.

REFERENCE 1

AUTHORS Pesch, M. and Schmitz, K.

TITLE Molecular cloning of a cDNA encoding for stachyose synthase from  
Stachys sieboldii

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 863)

AUTHORS Pesch, M.

TITLE Direct Submission

JOURNAL Submitted (13-AUG-2001) Pesch M., Botanisches Institut, LS3,  
Universitaet zu Koeln, Gyrhofstr. 15, D-50931 Koeln, GERMANY

FEATURES Location/Qualifiers

source

1..863

/organism="Stachys affinis"

/db\_xref="taxon:168825"

/tissue\_type="leaf"

/country="Japan"

Protein

1..863

/product="stachyose synthase"

/EC\_number="2.4.1.67"

CDS

1..863

/gene="sts"

/coded\_by="AJ344091.1:1..2592"

/db\_xref="GOA:Q8RW08"

/db\_xref="TrEMBL:Q8RW08"

ORIGIN

```

1  mapnpdpiss ifsplisvkk dnafelvvgk lsvknvplls eipsnvtfks fssicqssga
61  paplynraqs lsnccgflgf sqkesadsvt nslgkftnre fvsifrktw wstqwvgtsq
121 sdiqmetqwi mlnlpeiksy avvipivegk frsalfpgkd ghvlisaesg stcvkttstf
181 siayvhvsdn pytlmkdgyt avrvhldtfk lieeksappl vnkfgwctwd afyltvepag
241 iwngvkefsd ggfsprflii ddgwsinid gdpnedakn lvlggtqmta rlhrfdecek
301 frkykgsmm gpkvpyfdpk kpklliskai eiegvekard kaiqsgitdl sqyeiklkl
361 nkeldemfgg gndeckgssk gcsdcscskq nsgmkafnd lrtnfkglld iyvwhalaga
421 wgvkpgath lnakiepcckl spglgdgtmd lavvkilegs iglvhpdqae dfydsmsyl
481 skvgitgvkv dvihtleyvs enyggrvelg kayykglsks lknfnngsl issmqcndf
541 fllgteqism grvgddfwfq dpngdpmgvf wlqgvhmihc aynsmwmgqi ihpdwdmfqs
601 dhcsakfhag sraicggpvy vsdslgghdf dllklvfnd gtipkcihfa lptrdclfk
661 plfdsktilk iwnfnkyggv vgafncqgag wdpkeqrik ysecykplsg svhvsdiewd
721 qkveatkme aeeyavylte seklllttpe sdpiptlks ttfeifsfpv ikklgggvkf
781 apigltnlfn sggtiqgvvy degvakievk gdgkflayss svpkrsylng eeveykwsgn
841 gkvevdvpwy eecggisnit fvf

```

//



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search  for   

Limits

Preview/Index

History

Clipboard

Details

Show:

☐ 1: CAD20127. raffinose synthas...[gi:18181865][BLink](#), [Domains](#), [Links](#)

LOCUS CAD20127 798 aa linear PLN 15-JAN-2002

DEFINITION raffinose synthase [Pisum sativum].

ACCESSION CAD20127

VERSION CAD20127.2 GI:18181865

DBSOURCE embl locus PSA426475, accession [AJ426475.2](#)

KEYWORDS .

SOURCE Pisum sativum (pea)

ORGANISM Pisum sativumEukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;  
Pisum.

REFERENCE 1

AUTHORS Peterbauer,T., Mach,L., Mucha,J. and Richter,A.

TITLE Molecular characterization of raffinose synthase from pea (Pisum  
sativum L.) seeds

JOURNAL Unpublished

REFERENCE 2

AUTHORS Peterbauer,T.

TITLE Direct Submission

JOURNAL Submitted (02-JAN-2002) Peterbauer T., Institute of Ecology,  
University of Vienna, Althanstrasse 14, Vienna, A-1090, AUSTRIA

REMARK revised by [3]

REFERENCE 3 (residues 1 to 798)

AUTHORS Peterbauer,T.

TITLE Direct Submission

JOURNAL Submitted (09-JAN-2002) Peterbauer T., Institute of Ecology,  
University of Vienna, Althanstrasse 14, Vienna, A-1090, AUSTRIACOMMENT On Jan 16, 2002 this sequence version replaced [gi:18071125](#).

FEATURES

Location/Qualifiers

source

1..798

/organism="Pisum sativum"

/cultivar="Wunder von Kelvedon"

/db\_xref="taxon:3888"

/tissue\_type="seeds"

/country="Austria"

Protein

1..798

/product="raffinose synthase"

/EC\_number="2.4.1.82"

/function="galactinol:sucrose galactosyltransferase"

CDS

1..798

/gene="rfs"

/coded\_by="AJ426475.2:148..2544"

/db\_xref="GOA:Q8VWN6"

/db\_xref="TrEMBL:Q8VWN6"

ORIGIN

```

1  mappsitkta tqgdvistvd ignsplllsis ldqsrnflvn ghpfltqvpp nitttttstp
61  spfldfksnk dtiannntl qqqgcfvgfn tteakshhvv plgklkgikf tsifrkvvw
121 tthwvgtng elqhetqili ldknislgrp yvlllpilen sfrtslqppl ndyvdmsves
181 gsthvtgstf kaclylhln dpyrlvkeav kviqtklgtf ktleektpps iiekfgwctw
241 dafylkvhpq gwegvkalt dggcppgfvi iddgwqsish ddddpvterd gmnrtsageq
301 mpcrlikeye nykfreyeng dnggkkglvq fvrldkeefr svesvyvwha lcgywggvrp

```

361 kvcgmpeakv vvpklspgvk mtmedlavdk ivengvglvp pnlaqemfdg ihshlesagi  
421 dgvkvdvihl lellseeegg rvelakayyk altssvnhkf kgngviasme hcndffllgt  
481 eaislgrvgd dfwccdpdgd pngtywlqgc hmvhcaynsl wmgnfihpdw dmfqsthpc  
541 efhaasrais ggpvyvsdcv gnhnfkllks fvlpdgsilr cqhyalptrd clfedplhng  
601 ktmlkiwnln kyagvlglfn cggggwcpet rrnksasefs havtcyaspe diwcngktp  
661 mdikgvdvfa vyffkekklk lmkcsdrlev slepfsfelm tvsplkvfsk rliqfapigl  
721 vnmlnsggav qslefddas lvkigvrgcg elsvfasekp vcckidgvsv efdyedkmvr  
781 vqilwpgsst lslveflf

//

Disclaimer | Write to the Help Desk  
NCBI | NLM | NIH

May 6 2004 12:36:28